**IN THE SPECIFICATION:**

N.E. Please delete Tables 1-5, occurring on page 9 (lines 29-40) to page 39 (lines 1-40).

Please delete the paragraph starting on page 3 (lines 25-37) and continuing to page 4 (lines 1-15), and replace with the following paragraph:

--The present invention provides a composition of matter selected from: a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 2, 4, 6, 8, 16, 18; a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 10; a substantially pure or recombinant polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SEQ ID NO: 10; a natural sequence DCRS8 comprising mature SEQ ID NO: 10; a fusion polypeptide comprising DCRS8 sequence; a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 12 or 14; a substantially pure or recombinant polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SEQ ID NO: 12 or 14; a natural sequence DCRS9 comprising mature SEQ ID NO: 12 or 14; or a fusion polypeptide comprising DCRS9 sequence. Preferably, wherein the distinct nonoverlapping segments of identity include: one of at least eight amino acids; one of at least four amino acids and a second of at least five amino acids; at least three segments of at least four, five, and six amino acids, or one of at least twelve amino acids. In other embodiments, the: polypeptide: comprises a mature sequence of SEQ ID NO: 16 or 18; is an unglycosylated form of DCRS8 or DCRS9; is from a primate, such as a human; comprises at least seventeen amino acids of SEQ ID NO: 10 or 12; exhibits at least four nonoverlapping segments of at least seven amino acids of SEQ ID NO: 10 or 12; is a natural allelic variant of DCRS8 or DCRS9; has a length at least about 30 amino acids; exhibits at least two non-overlapping epitopes which are specific for a primate DCRS8 or DCRS9; is glycosylated; has a molecular weight of at least 30 kD with natural glycosylation; is a synthetic polypeptide; is attached to a solid substrate; is conjugated to another chemical

A1 Cmt

A1 cncld. moiety; is a 5-fold or less substitution from natural sequence; or is a deletion or insertion variant from a natural sequence.--

Please delete the paragraph on page 4 (lines 16-25) and replace with the following paragraph:

A2 --The invention further embraces a composition comprising: a substantially pure DCRS8 or DCRS9 and another cytokine receptor family member; a sterile DCRS8 or DCRS9 polypeptide; the DCRS8 or DCRS9 polypeptide and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration. Additional embodiments include a polypeptide comprising: mature protein sequence of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, and 18; a detection or purification tag, including a FLAG, His6, or Ig sequence; or sequence of another cytokine receptor protein. Kit embodiments include ones comprising a described polypeptide, and: a compartment comprising the protein or polypeptide; or instructions for use or disposal of reagents in the kit.--

Please delete the paragraph on page 4 (lines 26-36), continuing to page 5 (lines 1-2), and replace with the following paragraph:

A3 --Binding compositions are provided, e.g., comprising an antigen binding site from an antibody, which specifically binds to a natural DCRS8 or DCRS9 polypeptide, wherein: the binding compound is in a container; the DCRS8 or DCRS9 polypeptide is from a human; the binding compound is an Fv, Fab, or Fab2 fragment; the binding compound is conjugated to another chemical moiety; or the antibody: is raised against a peptide sequence of a mature polypeptide of SEQ ID NOS: 10, 12, or 14; is raised against a mature DCRS8 or DCRS9; is raised to a purified human DCRS8 or DCRS9; is immunoselected; is a polyclonal antibody; binds to a denatured DCRS8 or DCRS9; exhibits a Kd to antigen of at least 30 μM; is attached to a solid substrate, including a bead or plastic membrane; is in a sterile composition; or is detectably labeled, including a radioactive or fluorescent label. Kits include ones comprising such a binding compound, and: a compartment comprising the binding compound; or instructions for use or disposal of reagents in the kit.--

Please delete the paragraph on page 5 (lines 14-25) and replace with the following paragraph:

A4

--Nucleic acid compositions include an isolated or recombinant nucleic acid encoding a desribed polypeptide wherein the: DCRS8 or DCRS9 is from a human; or the nucleic acid: encodes an antigenic peptide sequence of SEQ ID NOS: 10, 12, or 14; encodes a plurality of antigenic peptide sequences of ; exhibits identity over at least thirteen nucleotides to a natural cDNA encoding the segment; is an expression vector; further comprises an origin of replication; is from a natural source; comprises a detectable label; comprises synthetic nucleotide sequence; is less than 6 kb, preferably less than 3 kb; is from a primate; comprises a natural full length coding sequence; is a hybridization probe for a gene encoding the DCRS8 or DCRS9; or is a PCR primer, PCR product, or mutagenesis primer. Also provided are a cell or tissue comprising such a recombinant nucleic acid, e.g., where the cell is: a prokaryotic cell; a eukaryotic cell; a bacterial cell; a yeast cell; an insect cell; a mammalian cell; a mouse cell; a primate cell; or a human cell.--

Please delete the paragraph on page 5 (lines 29-34) and replace with the following paragraph:

A5

--Other nucleic acids provided include ones which: hybridize under wash conditions of 30 minutes at 30° C and less than 2M salt to the coding portion of SEQ ID NO: 9 or 11; or exhibit identity over a stretch of at least about 30 nucleotides to a primate DCRS8 or DCRS9. Preferably, such will be nucleic acids where: the wash conditions are: at 45° C and/or 500 mM salt; at 55° C and/or 150 mM salt; or the stretch is at least 55 or 75 nucleotides.--

Please delete the paragraph on page 7 (lines 11-14) and replace with the following paragraph:

A6

--Nucleotide (SEQ ID NO: 1) and corresponding amino acid sequence (SEQ ID NO: 2) of a primate, e.g., human, DCRS6 coding segment is shown. Rodent, e.g., mouse, counterpart sequences are provided, e.g., SEQ ID NO: 3 and SEQ ID NO:4.--

Please delete the paragraph on page 7 (lines 15-20) and replace with the following paragraph:

A7

--Similarly, nucleotide (SEQ ID NO: 5) and corresponding amino acid sequence (SEQ ID NO: 6) of a primate, e.g., human, DCRS7 coding segment is shown. Rodent, e.g., mouse, counterpart sequences are provided, e.g., SEQ ID NO: 7 and SEQ ID NO: 8. Nucleotide (SEQ ID NO: 9) and corresponding amino acid sequence (SEQ ID NO: 10) of a primate, e.g., human, DCRS8 coding segment is shown.--

Please delete the paragraph on page 7 (lines 21-27) and replace with the following paragraph:

A8

--Nucleotide (SEQ ID NO: 11) and corresponding amino acid sequence (SEQ ID NO: 12) of a primate, e.g., human, DCRS9 coding segment is shown. Rodent, e.g., mouse, counterpart sequences are provided, e.g., SEQ ID NO: 13 and SEQ ID NO: 14. Nucleotide (SEQ ID NO: 15) and corresponding amino acid sequence (SEQ ID NO: 16) of a primate, e.g., human, DCRS10 coding segment is shown. Rodent, e.g., mouse, counterpart sequences are provided, e.g., SEQ ID NO: 17 and SEQ ID NO: 18.--

Please delete the paragraph on page 39 (lines 42-50) and replace with the following paragraph:

A9

--Table 1: Alignment of the cytoplasmic portions of various cytokine receptor subunits. The IL-17R_Hu (SEQ ID NO: 28) is GenBank AAB99730.1(U58917), gi|7657230; the IL-17R_Mu (SEQ ID NO: 29) is GenBank AAC52357.1(U31993), gi|6680411; the IL-17R_Ce (SEQ ID NO: 30) is GenBank AAA811100.1(U39997), gi|1353171; and the DCRS6_Ce (SEQ ID NO: 31) is EMBCAA90543.1(Z50177), gi|7503597. Of particular interest are motifs or features corresponding, in primate DCRS8 to: R/K at 339/340; D/E at 348/349; alpha helical regions from H353-Q365, C370-S381, E389-H396, K410-D414, and D485-H495; beta sheet regions correspond to F400-V404 and F458-Y462; E at 431; E/D at 442/443; Y/F at 458; D/E at 468-470; Y/F at 481; and Q/R/F at 523.--

Please delete the paragraph on page 41 (lines 1-5), and replace with the following paragraph:

--Table 1 shows comparison of the available sequences of primate, rodent, and various other receptors. Various conserved residues are aligned and indicated. The structurally homologous cytoplasmic domains most likely signal through pathways like IL-17, e.g., through NFkB. Similar to IL-1 signaling, it is likely that these receptors are involved in innate immunity and/or development.--

A10

Please delete the paragraph on page 41 (lines 6-21), and replace with the following paragraph:

--As used herein, the term DCRS shall be used to describe a protein comprising amino acid sequences shown in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, and 18 , respectively. In many cases, a substantial fragment thereof will be functionally or structurally equivalent, including, e.g., an extracellular or intracellular domain. The invention also includes a protein variation of the respective DCRS allele whose sequence is provided, e.g., a mutein or soluble extracellular construct. Typically, such agonists or antagonists will exhibit less than about 10% sequence differences, and thus will often have between 1 and 11 substitutions, e.g., 2-, 3-, 5-, 7-fold, and others. It also encompasses allelic and other variants, e.g., natural polymorphic, of the protein described. Typically, it will bind to its corresponding biological ligand, perhaps in a dimerized state with an alpha receptor subunit, with high affinity, e.g., at least about 100 nM, usually better than about 30 nM, preferably better than about 10 nM, and more preferably at better than about 3 nM. The term shall also be used herein to refer to related naturally occurring forms, e.g., alleles, polymorphic variants, and metabolic variants of the mammalian protein. Preferred forms of the receptor complexes will bind the appropriate ligand with an affinity and selectivity appropriate for a ligand-receptor interaction.--

A11

Please delete the paragraph on page 41 (lines 22-25), and replace with the following paragraph:

--This invention also encompasses combinations of proteins or peptides having substantial amino acid sequence identity with an amino acid sequence in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, or 18. It will include sequence variants with relatively few residue substitutions, e.g., preferably less than about 3-5.--

A12

Please delete the paragraph on page 42 (lines 1-22), and replace with the following paragraph:

--Amino acid sequence homology, or sequence identity, is determined by optimizing residue matches. In some comparisons, gaps may be introduces, as required. See, e.g., Needleham, et al., (1970) J. Mol. Biol. 48:443-453; Sankoff, et al., (1983) chapter one in Time Warps, String Edits, and Macromolecules: The Theory and Practice of Sequence Comparison, Addison-Wesley, Reading, MA; and software packages from IntelliGenetics, Mountain View, CA; and the University of Wisconsin Genetics Computer Group (GCG), Madison, WI; each of which is incorporated herein by reference. This changes when considering conservative substitutions as matches. Conservative substitutions typically include substitutions within the following groups: glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Homologous amino acid sequences are intended to include natural allelic and interspecies variations in the cytokine sequence. Typical homologous proteins or peptides will have from 50-100% homology (if gaps can be introduced), to 60-100% homology (if conservative substitutions are included) with an amino acid sequence segment of, e.g., SEQ ID NO: 10, 12, or 14. Homology measures will be at least about 70%, generally at least 76%, more generally at least 81%, often at least 85%, more often at least 88%, typically at least 90%, more typically at least 92%, usually at least 94%, more usually at least 95%, preferably at least 96%, and more preferably at least 97%, and in particularly preferred embodiments, at least 98% or more. The degree of homology will vary with the length of the compared segments. Homologous proteins or peptides, such as the allelic variants, will share most biological activities with the embodiments described in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, and 18.--

A13

Please delete the paragraph on page 44 (lines 11-26), and replace with the following paragraph:

--This invention contemplates use of isolated nucleic acid or fragments, e.g., which encode these or closely related proteins, or fragments thereof, e.g., to encode a corresponding polypeptide, preferably one which is biologically active. In addition, this invention covers isolated or recombinant DNAs which encode combinations of such proteins or polypeptides having characteristic sequences,

A14 Cont

e.g., of the DCRSs. Typically, the nucleic acid is capable of hybridizing, under appropriate conditions, with a nucleic acid sequence segment shown in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, and 17, but preferably not with a corresponding segment of other receptors described in Table 1. Said biologically active protein or polypeptide can be a full length protein, or fragment, and will typically have a segment of amino acid sequence highly homologous, e.g., exhibiting significant stretches of identity, to one shown in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, and 17. Further, this invention covers the use of isolated or recombinant nucleic acid, or fragments thereof, which encode proteins having fragments which are equivalent to the DCRS8 or DCRS9 proteins. The isolated nucleic acids can have the respective regulatory sequences in the 5' and 3' flanks, e.g., promoters, enhancers, poly-A addition signals, and others from the natural gene. Combinations, as described, are also provided.--

A14 cncld.

Please delete the paragraph beginning on page 46 (lines 19-37) and continuing to page 47 (lines 1-2), and replace with the following paragraph:

--Substantial identity in the nucleic acid sequence comparison context means either that the segments, or their complementary strands, when compared, are identical when optimally aligned, with appropriate nucleotide insertions or deletions, in at least about 60% of the nucleotides, generally at least 66%, ordinarily at least 71%, often at least 76%, more often at least 80%, usually at least 84%, more usually at least 88%, typically at least 91%, more typically at least about 93%, preferably at least about 95%, more preferably at least about 96 to 98% or more, and in particular embodiments, as high at about 99% or more of the nucleotides, including, e.g., segments encoding structural domains such as the segments described below. Alternatively, substantial identity will exist when the segments will hybridize under selective hybridization conditions, to a strand or its complement, typically using a sequence derived from SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, and 17. Typically, selective hybridization will occur when there is at least about 55% homology over a stretch of at least about 14 nucleotides, more typically at least about 65%, preferably at least about 75%, and more preferably at least about 90%. See, Kanehisa (1984) Nucl. Acids Res. 12:203-213, which is incorporated herein by reference. The length of homology comparison, as described, may be over longer stretches, and in certain embodiments will be over a stretch of at least about 17 nucleotides, generally at least about 20 nucleotides, ordinarily at least about 24 nucleotides, usually at least about 28 nucleotides,

A15 Cont

A15 cncld

typically at least about 32 nucleotides, more typically at least about 40 nucleotides, preferably at least about 50 nucleotides, and more preferably at least about 75 to 100 or more nucleotides. This includes, e.g., 125, 150, 175, 200, 225, 246, 273, and other lengths.--

Please delete the paragraph on page 48 (lines 23-26), and replace with the following paragraph:

A16

--As described above, the present invention encompasses primate DCRS6-10, e.g., whose sequences are disclosed in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, and 18, and described above. Allelic and other variants are also contemplated, including, e.g., fusion proteins combining portions of such sequences with others, including, e.g., epitope tags and functional domains.--

Please delete the paragraph on page 49 (lines 11-16), and replace with the following paragraph:

A17

--Candidate fusion partners and sequences can be selected from various sequence data bases, e.g., GenBank, c/o IntelliGenetics, Mountain View, CA; and BCG, University of Wisconsin Biotechnology Computing Group, Madison, WI, which are each incorporated herein by reference. In particular, combinations of polypeptide sequences provided in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, and 18 are particularly preferred. Variant forms of the proteins may be substituted in the described combinations.--

Please delete the paragraph beginning on page 51 (lines 30-37) and continuing to page 52 (lines 1-10), and replace with the following paragraph:

A18 Cmt

--A combination, e.g., including a DCRS8, of this invention can be used as an immunogen for the production of antisera or antibodies specific, e.g., capable of distinguishing between other cytokine receptor family members, for the combinations described. The complexes can be used to screen monoclonal antibodies or antigen-binding fragments prepared by immunization with various forms of impure preparations containing the protein. In particular, the term "antibodies" also encompasses antigen binding fragments of natural antibodies, e.g., Fab, Fab2, Fv, etc. The purified DCRS8 can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of

expression, or immunological disorders which lead to antibody production to the endogenous receptor. Additionally, DCRS8 fragments may also serve as immunogens to produce the antibodies of the present invention, as described immediately below. For example, this invention contemplates antibodies having binding affinity to or being raised against the amino acid sequences shown in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, and 18, fragments thereof, or various homologous peptides. In particular, this invention contemplates antibodies having binding affinity to, or having been raised against, specific fragments which are predicted to be, or actually are, exposed at the exterior protein surface of the native DCRS8 or DCRS9. Complexes of combinations of proteins will also be useful, and antibody preparations thereto can be made.--

A18 cncld.

Please delete the paragraph on page 52 (lines 26-31), and replace with the following paragraph:

A19

--DNA which encodes the protein or fragments thereof can be obtained by chemical synthesis, screening cDNA libraries, or by screening genomic libraries prepared from a wide variety of cell lines or tissue samples. Natural sequences can be isolated using standard methods and the sequences provided herein, e.g., in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, and 17. Other species counterparts can be identified by hybridization techniques, or by various PCR techniques, combined with or by searching in sequence databases, e.g., GenBank.--

Please delete the paragraph on page 60 (lines 11-18), and replace with the following paragraph:

A20

--A cytokine receptor protein that specifically binds to or that is specifically immunoreactive with an antibody generated against a defined immunogen, such as an immunogen consisting of the amino acid sequence of SEQ ID NO: 10, is typically determined in an immunoassay. The immunoassay typically uses a polyclonal antiserum which was raised, e.g., to a protein of SEQ ID NO: 10. This antiserum is selected to have low crossreactivity against other cytokine receptor family members, preferably from the same species, and any such crossreactivity is removed by immunoabsorption prior to use in the immunoassay.--

Please delete the paragraph on page 60 (lines 19-34), and replace with the following paragraph:

--In order to produce antisera for use in an immunoassay, the protein, e.g., of SEQ ID NO: 10, is isolated as described herein. For example, recombinant protein may be produced in a mammalian cell line. An appropriate host, e.g., an inbred strain of mice such as Balb/c, is immunized with the selected protein, typically using a standard adjuvant, such as Freund's adjuvant, and a standard mouse immunization protocol (see Harlow and Lane, supra). Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used an immunogen. Polyclonal sera are collected and titered against the immunogen protein in an immunoassay, e.g., a solid phase immunoassay with the immunogen immobilized on a solid support. Polyclonal antisera with a titer of $10^4$ or greater are selected and tested for their cross reactivity against other cytokine receptor family members using a competitive binding immunoassay such as the one described in Harlow and Lane, supra, at pages 570-573. Preferably at least two cytokine receptor family members are used in this determination. These cytokine receptor family members can be produced as recombinant proteins and isolated using standard molecular biology and protein chemistry techniques as described herein.--

A21

Please delete the paragraph on page 60 (lines 35-37), and continuing to page 61 (lines 1-6), and replace with the following paragraph:

--Immunoassays in the competitive binding format can be used for the crossreactivity determinations. For example, the protein of SEQ ID NO: 10 can be immobilized to a solid support. Proteins added to the assay compete with the binding of the antisera to the immobilized antigen. The ability of the above proteins to compete with the binding of the antisera to the immobilized protein is compared to the other proteins. The percent crossreactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% crossreactivity with each of the proteins listed above are selected and pooled. The cross-reacting antibodies are then removed from the pooled antisera by immunoabsorption with the above-listed proteins.--

A22

Please delete the paragraph on page 61 (lines 7-14), and replace with the following paragraph:

--The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein to the immunogen protein (e.g., the DCRS8 like protein of SEQ ID NO: 10). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required is less than twice the amount of the protein of the selected protein or proteins that is required, then the second protein is said to specifically bind to an antibody generated to the immunogen.--

A23

Please delete the paragraph on page 69 (lines 29-34), and replace with the following paragraph:

--PCR primers derived from the sequences are used to probe a human cDNA library. Sequences may be derived, e.g., from SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17, preferably those adjacent the ends of sequences. Full length cDNAs for primate, rodent, or other species DCRS8 are cloned, e.g., by DNA hybridization screening of λgt10 phage. PCR reactions are conducted using T. aquaticus Taqplus DNA polymerase (Stratagene) under appropriate conditions. Extending partial length cDNA clones is typically routine.--

A24

Please delete the paragraph on page 70 (lines 26-29), and replace with the following paragraph:

--Alternatively, two appropriate primers are selected from SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17. RT-PCR is used on an appropriate mRNA sample selected for the presence of message to produce a cDNA, e.g., a sample which expresses the gene.--

A25

Please delete the paragraph on page 73 (lines 33-37), and replace with the following paragraph:

--Primers specific for IL-17RA (Table 2) were designed and used in Taqman quantitative PCR against various human libraries. IL-17A is highly expressed in innate immune myeloid cells including dendritic cells and monocytes. Expression is also detected in T-cell libraries. These data

A26 amt

A26 demonstrate the receptor is expressed in immune cell types and may be regulated by activation conditions.--
cncld

Please delete the paragraph on page 74 (lines 1-3) and replace with the following paragraph:

A27 --Table 2: IL-17RA library description. CT for IL-17RA_H--

Please delete the paragraph on page 76 (lines 1-5), and replace with the following paragraph:

A28 --Primers specific for DCRS6_H (Table 3) were designed and used in Taqman quantitative PCR against various human libraries. DCRS6_H is expressed in innate immune myeloid cells including dendritic cells and monocytes. Expression is also detected in T-cell libraries. These data demonstrate the receptor is expressed in immune cell types and may be regulated by activation conditions.--

Please delete the paragraph on page 76 (lines 7-8) and replace with the following paragraph:

A29 --Table 3: DCRS6_H library description. CT for DCRS6_H.--

Please delete the paragraph on page 78 (lines 3-7), and replace with the following paragraph:

A30 --Primers specific for DCRS7_H (Table 4) were designed and used in Taqman quantitative PCR against various human libraries. DCRS6_H is expressed in innate immune myeloid cells including dendritic cells and monocytes. Expression is also detected in T-cell libraries. These data demonstrate the receptor is expressed in immune cell types and may be regulated by activation conditions.--

Please delete the paragraph on page 78 (lines 8-10) and replace with the following paragraph:

A31 --Table 4: DCRS7_H library description. CT for DCRS7_H --

Please delete the paragraph on page 80 (lines 3-6), and replace with the following paragraph:

A32

--Primers specific for DCRS9_H (Table 5) were designed and used in Taqman quantitative PCR against various human libraries. DCRS9_H is expressed in innate immune myeloid cells including dendritic cells and monocytes. Expression is also detected in T-cell libraries. These data demonstrate the receptor is expressed in immune cell types and may be regulated by activation conditions.--

Please delete the paragraph on page 80 (lines 7-9) and replace with the following paragraph:

A33

--Table 5: DCRS9_H library description. CT for DCRS9_H --

**IN THE CLAIMS:**

Please amend claims 1, 3, 5, 7, 12, and 16, as indicated below.

A34

1. (Once amended) A composition of matter selected from:
   a) a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 10;
   b) a substantially pure or recombinant polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SEQ ID NO: 10;
   c) a natural sequence DCRS8 comprising mature SEQ ID NO: 10;
   d) a fusion polypeptide comprising DCRS8 sequence;
   e) a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 12 or 14;
   f) a substantially pure or recombinant polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SEQ ID NO: 12 or 14;
   g) a natural sequence DCRS9 comprising mature SEQ ID NO: 12 or 14; or
   h) a fusion polypeptide comprising DCRS9 sequence.